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#2 OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/973,025

DATE: 12/04/2001
 TIME: 11:35:30

Input Set : N:\Crf3\RULE60\09973025.txt
 Output Set: N:\CRF3\12042001\I973025.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: MAERTENS, GEERT
 6 BOSMAN, FONS
 7 DE MARTYNOFF, GUY
 8 BUYSE, MARIE-ANGE

10 (ii) TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
 11 PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

13 (iii) NUMBER OF SEQUENCES: 111

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: NIXON & VANDERHYE P.C.
 17 (B) STREET: 1100 NORTH GLEBE ROAD
 18 (C) CITY: ARLINGTON
 19 (D) STATE: VIRGINIA
 20 (E) COUNTRY: U.S.A.
 21 (F) ZIP: 22201-4714

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/973,025
 C--> 31 (B) FILING DATE: 10-Oct-2001
 32 (C) CLASSIFICATION: 435

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/612,973
 36 (B) FILING DATE: 1996-03-11

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: BYRNE, THOMAS E.
 39 (B) REGISTRATION NUMBER: 32,205
 40 (C) REFERENCE/DOCKET NUMBER: 1487-10

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: (703) 816-4000
 44 (B) TELEFAX: (703) 816-4100

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 21 base pairs
 52 (B) TYPE: nucleic acid
 53 (C) STRANDEDNESS: single
 54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

58 (iii) HYPOTHETICAL: NO

C--> 60 (iv) ANTI-SENSE: NO

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

67 GGCATGCAAG CTTAATTAAAT T

69 (2) INFORMATION FOR SEQ ID NO: 2:

ENTERED

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Input Set : N:\Crf3\RULE60\09973025.txt
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71 (i) SEQUENCE CHARACTERISTICS:
72 (A) LENGTH: 68 base pairs
73 (B) TYPE: nucleic acid
74 (C) STRANDEDNESS: single
75 (D) TOPOLOGY: linear
77 (ii) MOLECULE TYPE: cDNA
79 (iii) HYPOTHETICAL: NO
C--> 81 (iv) ANTI-SENSE: NO
85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
87 CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT 60
89 TAACTGCA 68
91 (2) INFORMATION FOR SEQ ID NO: 3:
93 (i) SEQUENCE CHARACTERISTICS:
94 (A) LENGTH: 642 base pairs
95 (B) TYPE: nucleic acid
96 (C) STRANDEDNESS: single
97 (D) TOPOLOGY: linear
99 (ii) MOLECULE TYPE: cDNA
101 (iii) HYPOTHETICAL: NO
C--> 103 (iv) ANTI-SENSE: NO
106 (ix) FEATURE:
107 (A) NAME/KEY: CDS
108 (B) LOCATION: 1..639
110 (ix) FEATURE:
111 (A) NAME/KEY: mat_peptide
112 (B) LOCATION: 1..636
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
117 ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT 48
118 Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
119 1 5 10 15
121 CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG 96
122 Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
123 20 25 30
125 TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA 144
126 Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala
127 35 40 45
129 GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG 192
130 Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu
131 50 55 60
133 AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT 240
134 Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala
135 65 70 75 80
137 AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG 288
138 Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu
139 85 90 95
141 CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC 336
142 Leu Val Gly Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu
143 100 105 110
145 TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC 384

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Input Set : N:\Crf3\RULE60\09973025.txt
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146	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	
147		115			120						125						
149	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	
150	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	
151		130				135					140						
153	ATA	ACA	GGT	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	
154	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	
155	145					150				155				160			
157	ACA	ACG	GCC	GCC	CTG	GTG	GTA	TCG	CAG	CTG	CTG	CGG	ATC	CCA	CAA	GCT	GTC
158	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	
159						165				170			175				
161	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	
162	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	
163		180					185				190						
165	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	GTG	ATG	CTA	
166	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu	
167		195					200				205						
169	CTC	TTT	GCT	CTC	TAATAG										642		
170	Leu	Phe	Ala	Leu													
171		210															
174	(2)	INFORMATION FOR SEQ ID NO: 4:															
176	(i)	SEQUENCE CHARACTERISTICS:															
177	(A)	LENGTH: 212 amino acids															
178	(B)	TYPE: amino acid															
179	(D)	TOPOLOGY: linear															
181	(ii)	MOLECULE TYPE: protein															
183	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 4:															
185	Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	
186	1				5					10				15			
188	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	
189						20				25			30				
191	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	
192						35				40			45				
194	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	
195						50				55			60				
197	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	
198						65				70			75			80	
200	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu		
201							85				90			95			
203	Leu	Val	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu		
204						100				105			110				
206	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	
207						115				120			125				
209	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	
210						130				135			140				
212	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	
213						145				150			155			160	
215	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	
216						165				170			175				

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218 Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala
219 180 185 190
221 Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu
222 195 200 205
224 Leu Phe Ala Leu
225 210

228 (2) INFORMATION FOR SEQ ID NO: 5:

230 (i) SEQUENCE CHARACTERISTICS:
231 (A) LENGTH: 795 base pairs
232 (B) TYPE: nucleic acid
233 (C) STRANDEDNESS: single
234 (D) TOPOLOGY: linear

236 (ii) MOLECULE TYPE: cDNA

238 (iii) HYPOTHETICAL: NO

C--> 240 (iv) ANTI-SENSE: NO

243 (ix) FEATURE:

244 (A) NAME/KEY: CDS

245 (B) LOCATION: 1..792

247 (ix) FEATURE:

248 (A) NAME/KEY: mat_peptide

249 (B) LOCATION: 1..789

252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

254 ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
255 Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
256 1 5 10 15	
258 GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
259 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
260 20 25 30	
262 GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
263 Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
264 35 40 45	
266 ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
267 Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
268 50 55 60	
270 CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
271 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
272 65 70 75 80	
274 TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
275 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
276 85 90 95	
278 TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
279 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
280 100 105 110	
282 GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
283 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
284 115 120 125	
286 CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
287 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
288 130 135 140	

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290	GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
291	Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
292	145 150 155 160	
294	GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
295	Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
296	165 170 175	
298	TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
299	Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
300	180 185 190	
302	CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
303	Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
304	195 200 205	
306	TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA	672
307	Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro	
308	210 215 220	
310	CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG	720
311	Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala	
312	225 230 235 240	
314	GGT CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT	768
315	Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile	
316	245 250 255	
318	GTG ATG CTA CTC TTT GCT CCC TAATAG	795
319	Val Met Leu Leu Phe Ala Pro	
320	260	
323	(2) INFORMATION FOR SEQ ID NO: 6:	
325	(i) SEQUENCE CHARACTERISTICS:	
326	(A) LENGTH: 263 amino acids	
327	(B) TYPE: amino acid	
328	(D) TOPOLOGY: linear	
330	(ii) MOLECULE TYPE: protein	
332	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
334	Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
335	1 5 10 15	
337	Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
338	20 25 30	
340	Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
341	35 40 45	
343	Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
344	50 55 60	
346	Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
347	65 70 75 80	
349	Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
350	85 90 95	
352	Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
353	100 105 110	
355	Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
356	115 120 125	
358	Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
359	130 135 140	

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/973,025

DATE: 12/04/2001
TIME: 11:35:31

Input Set : N:\Crf3\RULE60\09973025.txt
Output Set: N:\CRF3\12042001\I973025.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:60 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:81 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:103 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:240 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:398 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:466 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:535 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:586 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
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L:2855 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3097 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3443 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3659 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:4723 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:4846 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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Input Set : N:\Crf3\RULE60\09973025.txt
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L:4986 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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